

Abstract: The invention relates to a method for analyzing cytosine methylations in DNA sequences, according to which non-methylated cytosines are first converted into uracil while 5-methylcytosine remains unmodified. The DNA is then amplified by means of a polymerase and at least one primer whose 5 end is connected to a probe via a linker. The probe is intramolecularly hybridized onto the amplified products in accordance with the methylation state of the DNA, hybridization being detectable via different detection systems. The inventive method is particularly suitable for diagnosing and predicting cancer diseases and other diseases associated with a modification of the methylation state as well as for predicting undesired effects of medicaments.